

IN THE SPECIFICATION:

Please replace paragraph beginning at page 16, line 1, with the following rewritten paragraph.

A¹
The cDNA and predicted amino acid sequences of AG1 and AG2 are shown in Figures 1A-1B and 2A-2B, respectively. Perfect and imperfect consensus polyadenylation signals are underlined and N-glycosylation sites are in bold face type. The DNA sequence of AG1 is also shown in SEQ ID NO: 1, while SEQ ID NO: 3 shows the complete DNA sequence of AG2. The predicted amino acid sequences for AG1 and AG2 are shown in SEQ ID NO: 2 and SEQ ID NO: 4, respectively.

Please replace paragraph beginning at page 16, line 7, with the following rewritten paragraph.

A²
As described in the examples, full-length *ag1*, depicted at nucleotide positions 8-394, inclusive, of Figure 1A, encodes a full-length AG1 protein of approximately 129 amino acids, shown as amino acids 1-129, inclusive, of Figure 1A (SEQ ID NO: 2). The 3' untranslated region is 945 nucleotides long, from positions 395-1338 of Figures 1A-1B (SEQ ID NO: 1). Imperfect polyadenylation signals occur at positions 1241-1245 and 1307-1311. The sequence (SEQ ID NO: 1) has been assigned GenBank Accession Number AF178459. The protein encoded by the predicted open reading frame (ORF) has a predicted molecular weight of about 15 kDa. The predicted isoelectric point is pH 9.6 and 44% of the predicted amino acid residues are hydrophobic. Two N-linked glycosylation sites have been identified at amino acid residues 36-38 and 71-73.

Please replace paragraph beginning at page 16, line 16, with the following rewritten paragraph.

A³
Full-length *ag2*, depicted at nucleotide positions 9-587, inclusive, of Figure 2A, encodes a full-length AG2 protein of approximately 193 amino acids, shown as amino acids 1-193, inclusive, of Figure 2A (SEQ ID NO: 4). The 3' untranslated region is 712 nucleotides long, from positions 588-1298 of Figures 2A-2B (SEQ ID NO: 4). Imperfect polyadenylation signals occur at positions 945-949 and 1141-1145. The sequence (SEQ ID NO: 3) has been assigned GenBank Accession Number AF178460. The protein encoded by the predicted open reading frame (ORF) has a predicted molecular weight of about 21.8 kDa. The predicted isoelectric point is pH 6.23 and 36% of the predicted amino acid residues are hydrophobic. Two N-linked glycosylation sites were identified at amino acid residues 36-38 and 51-53.